

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 18:03:05 ; Search time 23 Seconds

(without alignments)
640.178 Million cell updates/sec

Title: US-09-922-895-1

Perfect score: 1854
Sequence: 1 MTTSLDPTVETFTSTYDDV.....LERTSSVSPSTAPELSIVF 355

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	1854	100.0	355	1	PK1677 homo sapien
2	1717	92.6	355	1	PK6492 cercopithec
3	1706	92.0	355	1	PK6483 macaca mula
4	1293	69.7	359	1	PK1678 mus musculus
5	1264	68.2	359	1	PK1678 mus musculus
6	1253.5	67.6	359	1	PK1678 mus musculus
7	1181.5	63.7	355	1	PK1678 mus musculus
8	1121.5	60.5	355	1	PK1678 mus musculus
9	1114.5	60.1	355	1	PK1678 mus musculus
10	863.5	52.0	373	1	PK1678 mus musculus
11	955.5	51.5	373	1	PK1678 mus musculus
12	954	51.2	360	1	PK1678 mus musculus
13	949.5	51.2	352	1	PK1678 mus musculus
14	948	51.1	352	1	PK1678 mus musculus
15	947.5	51.1	352	1	PK1678 mus musculus
16	945.5	50.9	352	1	PK1678 mus musculus
17	944.5	50.9	352	1	PK1678 mus musculus
18	943	50.8	354	1	PK1678 mus musculus
19	942.5	50.8	352	1	PK1678 mus musculus
20	940.5	50.7	352	1	PK1678 mus musculus
21	940.5	50.7	352	1	PK1678 mus musculus
22	940.5	50.7	352	1	PK1678 mus musculus
23	940	50.7	354	1	PK1678 mus musculus
24	939.5	50.7	352	1	PK1678 mus musculus
25	939.5	50.7	352	1	PK1678 mus musculus
26	939.5	50.7	352	1	PK1678 mus musculus
27	938.5	50.6	352	1	PK1678 mus musculus
28	927.5	50.0	356	1	PK1678 mus musculus
29	886.5	47.8	374	1	PK1678 mus musculus
30	803.5	43.3	360	1	PK1678 mus musculus
31	780.5	42.1	360	1	PK1678 mus musculus
32	710.5	38.3	354	1	PK1678 mus musculus
33	703	37.9	356	1	PK1678 mus musculus

34	698.5	37.7	354	1	C3X1_MOUSE	Q92093 mus musculus
35	692.5	37.4	355	1	CKR8_HUMAN	P51683 homo sapien
36	684	36.9	355	1	C3X1_HUMAN	P49238 homo sapien
37	659	35.5	353	1	CKR8_MOUSE	P56484 mus musculus
38	579.5	31.3	384	1	CKR6_HUMAN	O00590 homo sapien
39	572	30.9	374	1	CKR6_HUMAN	P51684 homo sapien
40	565	30.5	367	1	CKR6_MOUSE	O54683 mus musculus
41	563	30.4	357	1	CKR9_HUMAN	P51686 homo sapien
42	541.5	29.2	378	1	CKR7_HUMAN	P32248 homo sapien
43	541	29.2	369	1	CKR9_MOUSE	O98707 mus musculus
44	529.5	28.6	378	1	CKD6_MOUSE	O08410 mus musculus
45	523.5	28.2	367	1	CKR3_MOUSE	

ALIGNMENTS

RESULT 1
ID CKR3_HUMAN STANDARD; PRT; 355 AA.
AC P51677; Q15748; Q9ULY8;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3) (CCR3)
DE (CKR3) (Eosinophil eotaxin receptor).
GN CKR3 OR CCR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Monocytes;
RX MEDLINE=95348056; PubMed=7622448;
RT Combadiere C., Ahuja S.K., Murphy P.M.;
RT "Cloning and functional expression of a human eosinophil CC chemokine
RT receptor.";
RT J. Biol. Chem. 270:16491-16494(1995).
RN [2]
RP ERRATUM.
RX Combadiere C., Ahuja S.K., Murphy P.M.;
RX J. Biol. Chem. 270:30235-30235(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96235044; PubMed=8642344;
RX Daugherty B.L., Siciliano S.J., Demartino J.A., Malkowitz L.,
RX Stotova A., Springer M.S.;
RX "Cloning, expression, and characterization of the human eosinophil
RX eotaxin receptor.";
RX J. Exp. Med. 183:2349-2354(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=96281895; PubMed=8676064;
RX Ponath P.D., Qin S., Post T.W., Wang J., Wu L., Gerard N.P.,
RX Newman W., Gerard C., Mackay C.R.;
RX "Molecular cloning and characterization of a human eotaxin receptor
RX expressed selectively on eosinophils.";
RX J. Exp. Med. 183:2737-2748(1996).
RN [5]
RP SEQUENCE FROM N.A.
RX Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lai R.;
RX "Partial resistance to infection by syncytium-inducing primary HIV-1
RX in exposed uninfected individuals homozygous for CCR5 32bp deletion.";
RX Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. AND VARIANT SER-218.
RX MEDLINE=21040311; PubMed=11196669;
RX Kato H., Tsuchiya N., Izumi S., Miyama M., Nakajima T., Kawasaki H.,
RX Hirai K., Tokunaga K.;
RX "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RX Genes Immun. 1:97-104(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,

	CC	ectatin-3, MCP-3, MCP-4, RANTES and MIP-1 delta. Subsequently transduces a signal by increasing the intracellular calcium ions level. Alternative coreceptor with CD4 for HIV-1 infection.
	CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
	CC	-1- TISSUE SPECIFICITY: IN EOSINOPHILS AS WELL AS TRACE AMOUNTS IN NEUTROPHILS AND MONOCYTES.
	CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@lsb-sib.ch).
	CC	
DR	EMBL	U28694; AAC50469.1; -
DR	EMBL	U51241; AAB16831.1; -
DR	EMBL	O49727; AAB09726.1; -
DR	EMBL	AF026535; AAB82589.1; -
DR	EMBL	AB023887; BAA6964.1; -
DR	Genev	HGNC:1604; CCR3.
DR	MIM	601268; -
DR	InterPro	IPR000276; GPCR_Rhodpsn.
DR	Pfam	PF00001; 7tm_1; 1.
DR	PRINTS	PR00237; GPCRRHODOPSN.
DR	PROSITE	PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR	PROSITE	PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW		G-protein coupled receptor; Transmembrane; Polymorphism.
FT	DOMAIN	1 34 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	35 62 1 (POTENTIAL).
FT	DOMAIN	63 72 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	73 93 2 (POTENTIAL).
FT	DOMAIN	94 107 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	108 129 3 (POTENTIAL).
FT	DOMAIN	130 146 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	147 171 4 (POTENTIAL).
FT	DOMAIN	172 203 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	204 223 5 (POTENTIAL).
FT	DOMAIN	224 239 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	240 264 6 (POTENTIAL).
FT	DOMAIN	265 281 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	282 305 7 (POTENTIAL).
FT	DOMAIN	306 355 CYTOPLASMIC (POTENTIAL).
FT	DISULFID	106 183 BY SIMILARITY.
FT	VARIANT	218 218 C-> S (REDUCED FUNCTION). /FTD-VAR_010668.
FT	CONFLICT	276 276 S-> T (IN REF. 4 AND 5).
SQ	SEQUENCE	355 AA; 41043 MW; E95DCD7A6C643874 CRC64;
	Query Match	100.0%; Score 1854; DB 1; Length 355;
	Best Local Similarity	100.0%; Pred. No. 1.4e-96;
	Matches 355; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Dy	1	MTTSIDVPEFGTSTSYDDVGALCEKADTRALMAQFPVPLXSIVTFVGLGNVVVMILI 60 1 MTSSIDVPEFGTSTSYDDVGALCEKADTRALMAQFPVPLXSIVTFVGLGNVVVMILI 60
Dd	61	KYRRLRIKNTNYLLNLAIASDLFLVTLPEFWIHYRGHWVGRHGCKLSGFYHTGLYSE 120 61 KYRRLRIKNTNYLLNLAIASDLFLVTLPEFWIHYRGHWVGRHGCKLSGFYHTGLYSE 120
Dd	61	KYRRLRIKNTNYLLNLAIASDLFLVTLPEFWIHYRGHWVGRHGCKLSGFYHTGLYSE 120 61 KYRRLRIKNTNYLLNLAIASDLFLVTLPEFWIHYRGHWVGRHGCKLSGFYHTGLYSE 120
Dd	121	IFFIIILLIDRYLAIVHAVFALRARATVEFGYITSIVTGWLVAIALPERIFYETEEELPEE 180 121 IFFIIILLIDRYLAIVHAVFALRARATVEFGYITSIVTGWLVAIALPERIFYETEEELPEE 180
Dd	121	IFFIIILLIDRYLAIVHAVFALRARATVEFGYITSIVTGWLVAIALPERIFYETEEELPEE 180 121 IFFIIILLIDRYLAIVHAVFALRARATVEFGYITSIVTGWLVAIALPERIFYETEEELPEE 180
Dd	181	TLCGSAIYPEDTVYSWRHEHTLRMTFCVLPLLVLAICYGTGIITKLRCSPKKKYKAIRL 240 181 TLCGSAIYPEDTVYSWRHEHTLRMTFCVLPLLVLAICYGTGIITKLRCSPKKKYKAIRL 240
Dd	181	TLCGSAIYPEDTVYSWRHEHTLRMTFCVLPLLVLAICYGTGIITKLRCSPKKKYKAIRL 240 181 TLCGSAIYPEDTVYSWRHEHTLRMTFCVLPLLVLAICYGTGIITKLRCSPKKKYKAIRL 240
Dd	241	IFVIMAVFEIWTPTNNAILISVSQSILFGNDCESKRLDVMLVTGVIAIASHCGMNPVI 300 241 IFVIMAVFEIWTPTNNAILISVSQSILFGNDCESKRLDVMLVTGVIAIASHCGMNPVI 300
Dd	241	IFVIMAVFEIWTPTNNAILISVSQSILFGNDCESKRLDVMLVTGVIAIASHCGMNPVI 300 241 IFVIMAVFEIWTPTNNAILISVSQSILFGNDCESKRLDVMLVTGVIAIASHCGMNPVI 300

ID	CDR3_CERAE	STANDARD:	PRT:	355 AA.
AC	P56492:			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3) (CCR3)			
DE	(CCR3).			
GN	CCR3 OR CCKBR3.			
OS	Cercopithecus aethiops (Green monkey) (Grivet)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
OC	Cercopithecinae; Cercopithecus.			
OX	NCBI_TaxID=9534;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	SOI N., Treboute C., Gomas E., Ferchal F., Allison M.;			
RL	Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.			
CC	-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,			
CC	MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY			
CC	INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL, Y13775; CAA74106.1; -			
DR	InterPro: IPR000276; GPCR_Rhodpsn.			
DR	InterPro: IPR001230; Prenyl_site.			
DR	Pfam: PF00001; 7tm.1; 1.			
DR	PRINTS: PR00237; GPCRHHODPSN.			
DR	PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.			
DR	PROSITE: PS0262; G_PROTEIN_RECPT_FL_2; 1.			
KW	G-protein coupled receptor; Transmembrane.			
FT	DOMAIN 1			
FT	TRANSMEM 35			
FT	TRANSMEM 62			
FT	DOMAIN 72			
FT	TRANSMEM 73			
FT	TRANSMEM 94			
FT	DOMAIN 108			
FT	TRANSMEM 129			
FT	DOMAIN 130			
FT	TRANSMEM 147			
FT	TRANSMEM 171			
FT	DOMAIN 172			
FT	TRANSMEM 204			
FT	DOMAIN 224			
FT	TRANSMEM 240			
FT	TRANSMEM 264			
FT	DOMAIN 281			
FT	TRANSMEM 282			
FT	TRANSMEM 306			
FT	DISULFID 106			
FT	DISULFID 183			
FT	SEQUENCE 355 AA;			
FT	SEQUENCE 4467A5EFEBB978FP CMC64;			
SO	SEQUENCE			
QY	Query Match	92.6%	Score 1717, DB 1:	Length 355;
QY	Best Local Similarity	92.1%	Pred. No. 7.6e-91;	
QY	Matches 327; Conservative 13; Mismatches 15; Indels 0; Gaps 0;			
DB	1 MTSISDVTETGTSYDDVGLCEKADTRALMAQFVPLSLVFTVGLGAVVYVMTLI 60			
DB	1 MTSISVYETGEPSTYDDMGGLCEKAVGALINQFVPLSLVFTVGLGAVVYVMTLI 60			

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OY 61 KYRLRLIMNTIYLNLAIASDLLEFLVTLPRHIVYRGHNWFGHGKCKLSGFIHTGLYSE 120
DB 61 KYRLRLIMNTIYLNLAIASDLLEFLVTLPRHIVYRGHNWFGHGKCKLSGFIHTGLYSE 120
OY 121 IFFIILLTDRIYLAIVHAFALRARTVETGVTISITWGLAVLAALPEFIETEELEFEE 180
DB 121 IFFIILLTDRIYLAIVHAFALRARTVETGVTISITWGLAVLAALPEFIETEELEFEE 180
OY 181 TLCSALYPEDVYSWRHFTLMTIFCLVPLLVNAICVTGIIKTLRCPSSKKRYAIRL 240
DB 181 TLCSALYPEDVYSWRHFTLMTIFCLVPLLVNAICVTGIIKTLRCPSSKKRYAIRL 240
OY 241 IFVIMAVFEFTFPYVNAIILSSYQSLFENDCKSKHDLVMTLVETVAISHCCNAPYI 300
DB 241 IFVIMAVFEFTFPYVNAIILSSYQSLFENDCKSKHDLVMTLVETVAISHCCNAPYI 300
OY 301 YAFVGERFRKYLHFFRHLMLHGRYIPFLPSEKLEKERTSSVSPSTAEPELSIVF 355
DB 301 YAFVGERFRKYLHFFRHLMLHGRYIPFLPSEKLEKERTSSVSPSTAEPELSIVF 355

RESULT 3
CKR3_MACMU STANDARD; PRT: 355 AA.
ID AC P56483:
DT 15-JUL-1998 (rel. 36, Created)
DT 15-JUL-1998 (rel. 36, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR3)
DE (CCR3).
GN CCR3 OR CCKBR3.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_Taxid=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT Identification and comparison of eleven rhesus macaque chemokine
RT receptors.*;
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98118446; PubMed=9454694;
RA Sol N., Treboutte C., Gomas E., Ferchal F., Shacklett B., Alizon M.;
RT The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor
RT for HIV-2, but not for HIV-1.*;
RL Virology 240:213-220(1998).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,
CC MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL: AF017283; AAB70527.1; -
CC EMBL: Y13776; CAA74107.1; -
CC InterPro: IPR000276; GPCR_Rhodopsin.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS: PR00237; GPCR_Rhodopsin.
CC PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 35 62 1 (POTENTIAL).
FT DOMAIN 63 72 2 (POTENTIAL).
FT TRANSMEM 73 93 3 (POTENTIAL).
FT DOMAIN 94 107 4 (POTENTIAL).
FT TRANSMEM 108 129 5 (POTENTIAL).
FT DOMAIN 130 146 6 (POTENTIAL).
FT TRANSMEM 147 171 7 (POTENTIAL).
FT DOMAIN 172 203 8 (POTENTIAL).
FT TRANSMEM 204 223 9 (POTENTIAL).
FT DOMAIN 224 239 10 (POTENTIAL).
FT TRANSMEM 240 264 11 (POTENTIAL).
FT DOMAIN 265 281 12 (POTENTIAL).
FT TRANSMEM 282 305 13 (POTENTIAL).
FT DOMAIN 306 335 14 (POTENTIAL).
FT DISULFID 106 183 15 (POTENTIAL).
FT CONFLICT 180 180 K -> E (IN REF. 2).
FT CONFLICT 202 202 K -> R (IN REF. 2).
SQ SEQUENCE 355 AA: 40805 MW: 4271 E69497099F CRC64;

Query Match 92.0%; Score 1706; DB 1; Length 355;
Best Local Similarity 91.3%; Pred. No. 3.2e-90;
Matches 324; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

OY 1 MTSIDTVETFEFTSYDDVGLCEKADRALMAQFVPPPLSYLFTVGLGNVVMIL 60
DB 1 MTSIDTVETFEFTSYDDVGLCEKADRALMAQFVPPPLSYLFTVGLGNVVMIL 60
OY 61 KYRLRLIMNTIYLNLAIASDLLEFLVTLPRHIVYRGHNWFGHGKCKLSGFIHTGLYSE 120
DB 61 KYRLRLIMNTIYLNLAIASDLLEFLVTLPRHIVYRGHNWFGHGKCKLSGFIHTGLYSE 120
OY 121 IFFIILLTDRIYLAIVHAFALRARTVETGVTISITWGLAVLAALPEFIETEELEFEE 180
DB 121 IFFIILLTDRIYLAIVHAFALRARTVETGVTISITWGLAVLAALPEFIETEELEFEE 180
OY 181 TLCSALYPEDVYSWRHFTLMTIFCLVPLLVNAICVTGIIKTLRCPSSKKRYAIRL 240
DB 181 TLCSALYPEDVYSWRHFTLMTIFCLVPLLVNAICVTGIIKTLRCPSSKKRYAIRL 240
OY 241 IFVIMAVFEFTFPYVNAIILSSYQSLFENDCKSKHDLVMTLVETVAISHCCNAPYI 300
DB 241 IFVIMAVFEFTFPYVNAIILSSYQSLFENDCKSKHDLVMTLVETVAISHCCNAPYI 300
OY 301 YAFVGERFRKYLHFFRHLMLHGRYIPFLPSEKLEKERTSSVSPSTAEPELSIVF 355
DB 301 YAFVGERFRKYLHFFRHLMLHGRYIPFLPSEKLEKERTSSVSPSTAEPELSIVF 355

RESULT 4
CKR3_MOUSE STANDARD; PRT: 359 AA.
ID AC P51678:
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE Probable C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR3)
DE (CCR3) (CCR3) (Macrophage inflammatory protein-1 alpha receptor-like
DE 2) (MIP-1 alpha R12).
GN CCR3 OR CCKBR3 OR CCKBR1L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SV.
RX MEDLINE=96072806; PubMed=7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA Gerard C.;
RT Molecular characterization of two murine eosinophil beta chemokine
RT receptors.*;
RL J. Immunol. 155:5299-5305(1995).
RN [2]

```

SEQUENCE FROM N.A.

RC STRAIN-129/SVJ; PubMed=7542241;

RA Gao J.-L., Murphy P.M.;

RT "Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.";

RL J. Biol. Chem. 270:17494-17501(1995).

CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN, MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: DETECTED IN SKELETAL MUSCLE AND IN TRACE AMOUNTS IN LEUKOCYTES.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL: U29677; AAA86118.1; -

DR EMBL: U28406; AAA89155.1; -

DR MGI:104616; Gmbr112.

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCR_RHODOPSN.

DR PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.

DR PROSITE: PS50262; G_PROTEIN_REC_P1.2; 1.

KM G-protein coupled receptor; Transmembrane.

FT DOMAIN 1 38

FT TRANSSEM 39 64

FT DOMAIN 65 68

FT TRANSSEM 69 95

FT DOMAIN 96 111

FT TRANSSEM 112 133

FT DOMAIN 134 150

FT TRANSSEM 151 175

FT DOMAIN 176 201

FT TRANSSEM 202 227

FT DOMAIN 228 243

FT TRANSSEM 244 268

FT DOMAIN 269 285

FT TRANSSEM 286 309

FT DOMAIN 310 359

FT DISULFID 110 187

FT CONFLICT 270 270

SO SEQUENCE 359 AA; 41825 MM; AC11ED66E283CEAF CRC64;

Query Match 69.7%; Score 1293; DB 1; Length 359;

Best Local Similarity 70.4%; Pred. No. 7e-67;

Matches 245; Conservative 41; Mismatches 62; Indels 0; Gaps 0;

QY 8 VETGTSYNDVCLCEKADPTALMAQFVPLISVTVGLGNYVVMILIKRRRI 67

DB 12 VESETTPEYEMAPPEKAKIKELGSLPLPLSLVFILGLNMVALLIKYRKLOI 71

QY 68 MTNIIYLAISDLFTLVLPFMIHYVGNHNVFGHGCKLLSGFYHGLSEIFILL 127

DB 72 MTNIIYLAISDLFTLVLPFMIHYVGNHNVFGHGCKLLSGFYHGLSEIFILL 131

QY 128 TIDRYLAIVHVAFLRATVTEGVTISVWGLAVLALPEFIYEETEEELCSALY 187

DB 132 TIDRYLAIVHVAFLRATVTEGVTISVWGLAVLALPEFIYEETEEELCSALY 191

QY 188 PEDVYVSRHRTIATIFCLVPLVVAICTYTGIIKTLRCPSSKKYKATRLIFVMAV 247

DB 192 PEGEEDSWKRHRLRMIFGLALPLVAVICYSIGIKTLRCPSSKKYKATRLIFVMAV 251

QY 248 FFIWTPYNAVLILSSVSLFGNDCERSKHLDMVLVTEVIAVSHCCMNVIYAFVGR 307

DB 252 FFIWTPYNAVLILSSVSLFGNDCERSKHLDMVLVTEVIAVSHCCMNVIYAFVGR 311

QY 308 FRKYLRFHRLMHLGRYIPLPSEKLETTSSSPSTAPELISV 355

DB 312 FRKYLRFHRLMHLGRYIPLPSEKLETTSSSPSTAPELISV 359

RESULT 5

CR3_RAT

ID CR3_RAT STANDARD; PRT; 359 AA.

AC 054814; OS5169; (rel. 39, Created)

DT 30-MAY-2000 (rel. 39, Last sequence update)

DR 30-MAY-2000 (rel. 39, Last annotation update)

DE C-C chemokine receptor type 3 (C-C CR-3) (CCR-3) (CCR3)

GN CCR3 OR CCR3R3.

OS Rattus norvegicus (rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_Taxid=10116;

RN [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RC STRAIN-Wistar; TISSUE-Spleen;

RX MEDLINE-98318173; PubMed=9653467;

RA Jiang Y., Salazar M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,

RT "Chemokine receptor expression in cultured glia and rat experimental allergic encephalomyelitis.";

RT J. Neuroimmunol. 86:1-12(1998).

RM [2]

RP SEQUENCE FROM N.A.

RC STRAIN-Wistar; TISSUE-Spleen;

RA Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;

RL Submitted (Jan-1998) to the EMBL/Genbank/DDBJ databases

CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN, MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN SPLEEN BUT NOT IN ASTROCYTES OR MICROGLIA.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL: AF003954; AAC03337.1; -

DR EMBL: Y13400; CAAT3830.1; -

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCR_RHODOPSN.

DR PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.

DR PROSITE: PS50262; G_PROTEIN_REC_P1.2; 1.

KM G-protein coupled receptor; Transmembrane.

FT DOMAIN 1 43

FT TRANSSEM 44 64

FT DOMAIN 65 74

FT TRANSSEM 75 95

FT DOMAIN 96 112

FT TRANSSEM 113 133

FT DOMAIN 134 154

FT TRANSSEM 155 175

FT DOMAIN 176 206

FT TRANSSEM 207 227

FT DOMAIN 228 243

FT TRANSSEM 244 264

FT DOMAIN 265 288

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

POTENTIAL.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

POTENTIAL.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

POTENTIAL.

EXTRACELLULAR (POTENTIAL).

DT 01-OCF-1993 (Rel. 27, Created)
DT 01-OCF-1993 (Rel. 27, Last sequence update)
DT 16-OCF-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 1 (C-C CR-1) (CC-CR-1) (CCR-1) (CCR1)
DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
DE (RANTES-R) (HM145) (LD78 receptor).
DE CCR1 OR CCR1R1 OR CCR1L
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SOURCE FROM N.A.
RX MEDLINE=93161416; PubMed=7679328;
RA Neote K., Digregorio D., Mak Y.Y., Horuk R., Schall T.J.;
RT "Molecular cloning, functional expression, and signaling
characteristics of a C-C chemokine receptor.";
RL Cell 72:415-425(1993).

```

RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-93240122; PubMed-7683036;
RA Gao J.-L., Kuhn D., Tiffany H.L., McDermott D., Li X., Francke U.,
RT Murphy P.M.;
RT "Structure and functional expression of the human macrophage
RT inflammatory protein 1 alpha/RANTES receptor."
RL J. Exp. Med. 177:1421-1427(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE-Monocytes; PubMed-7505609;
RA MEDLINE-94092629;
RA Nomura H., Nielsen B.W., Matsushima K.;
RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
RT leukocyte chemotactic peptide receptors."
RL Int. Immunol. 5:1239-1249(1993).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1 DELTA, RANTES, AND MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-
CC BETA OR MCP-1 AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING
CC THE INTRACELLULAR CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING
CC STEM CELL PROLIFERATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT HEMATOPOIETIC
CC CELLS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; L09230; AAA58408.1;
DR EMBL; L10918; AAA36543.1;
DR EMBL; D10925; BAA01723.1;
DR PIR; A45177; A45177.
DR GENE; HGNC:1602; CCR1.
DR MIM; 601159;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.
DR PROSITE; PS50262; G_PROTEIN_REC_P1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 34
FT TRANSMEM 1 34
FT TRANSMEM 35 60
FT DOMAIN 61 64
FT TRANSMEM 65 91
FT TRANSMEM 92 107
FT TRANSMEM 108 129
FT TRANSMEM 130 146
FT TRANSMEM 147 171
FT TRANSMEM 172 197
FT TRANSMEM 198 223
FT TRANSMEM 224 239
FT TRANSMEM 240 264
FT TRANSMEM 265 281
FT TRANSMEM 282 305
FT TRANSMEM 306 335
FT CARBOHYD 5
FT DISULFID 106
FT CONFLICT 337
FT SEQUENCE 355 AA; 41172 MW; B2C100FED275985 CRC64;
Query Match 63.7%; Score 1181.5; DB 1; Length 355;
Best Local Similarity 63.2%; Pred. No. 1.4e-60;
Matches 222; Conservative 57; Mismatches 71; Indels 1; Gaps 1;
OY 6 DTVEFGTSTYYD-DVGLLCEKADTRALMAQFVPLPVLTGVLGNVVVVMLIKRKR 64
Db 5 NTFEDYDTTFEFYGDGATPCQKVNBRARAGQALPLPLVSLVGVIGLVAVLVAVYQKR 64

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OY 65 LRMNTNIVLNLAIISDLLFLVTLPPWVHVRGNHVFQHGCKLLSGEYHGLYSEIFFI 124
Db 65 LKMTSTIYLNLAISDLLFLFLPMDIKLDQVDFGDMCKILSGEYHGLYSEIFFI 124
OY 125 ILTIDRVLATVHAFAFARVNTGCVTSITVWGLAVLAALPEIFETETLFEETICS 184
Db 125 ILTIDRVLATVHAFAFARVNTGCVTSITVWGLAVLAALPEIFETETLFEETICS 184
OY 185 ALPEDTVYVSWRHEFTLMTIFCLVPLVNAICVTGAIKTLRCPSKKRYKARILFYI 244
Db 185 LHPFHSLREKMLFQALKNLNFGVLPLVIMICTGIIKILRRPNRKSRAVAILFYI 244
OY 245 MAVFIFETPVVAILLSYGSLFQNDCKSRHLDVNLVTEYIAYSHCCNPIYIAFV 304
Db 245 MIIFLFETPVVAILLSYGSLFQNDCKSRHLDVNLVTEYIAYSHCCNPIYIAFV 304
OY 305 GREFKRYLRHPRHLNHLGTYIFPLPSEKTEKRTSSPSPAEELISVF 355
Db 305 GREFKRYLRHPRHLNHLGTYIFPLPSEKTEKRTSSPSPAEELISVF 355
OY 305 GERFKRYLRHPRHLNHLGTYIFPLPSEKTEKRTSSPSPAEELISVF 355
Db 305 GERFKRYLRHPRHLNHLGTYIFPLPSEKTEKRTSSPSPAEELISVF 355

RESULT 8
ID CKR1_MACMU STANDARD; PRT; 355 AA.
AC P56482;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 1 (C-C CKR-1) (CC-CKR-1) (CCR-1) (CCR1).
GN CCR1 OR CCR1R1.
OS Macaca mulatta (rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21354176; PubMed-11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC RANTES, MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
CC PROLIFERATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF017282; AAB70526.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.
DR PROSITE; PS50262; G_PROTEIN_REC_P1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 34
FT TRANSMEM 35 60
FT TRANSMEM 61 64
FT TRANSMEM 65 91
FT TRANSMEM 92 107
FT TRANSMEM 108 129
FT TRANSMEM 130 146
FT DOMAIN 130 146
FT CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMAIN 224 239 5 (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 335 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
SQ SEQUENCE 355 AA; 41198 MW; 41CAEA7CC19D2304 CRC64;

Query Match 60.5%; Score 1121.5; DB 1; Length 355;
Best Local Similarity 60.4%; Pred. No. 3,4e-57;
Matches 216; Conservative 55; Mismatches 77; Indels 7; Gaps 2;

QY 8 VETFGTSTYD-----DVG--LLCEKADTRALMAQFPPPLYSIVFTVGLGNVVMILLI 60
DB 1 METPNTEDYDMDTEPDYGDATPCGHKYNERRAILAQLEPLYSIVFTVGLGNVLMVLV 60
QY 61 KYRRLRLMTNIVLNLTAISDLLELVLPFWIHVYRGHNVFGHGMCKILSGFHTGLYSE 120
DB 61 QYRRLKMTNIVLNLTAISDLLELVLPFWIHVYRGHNVFGHGMCKILSGFHTGLYSE 120
QY 121 IFTTILITDRYLAIVHAVPALARKYTFEGVITSYWGIAVLAALPEFTFYETEEELFEE 180
DB 121 IFTTILITDRYLAIVHAVPALARKYTFEGVITSYWGIAVLAALPEFTFYETEEELFEE 180
QY 121 IFTTILITDRYLAIVHAVPALARKYTFEGVITSYWGIAVLAALPEFTFYETEEELFEE 180
DB 121 IFTTILITDRYLAIVHAVPALARKYTFEGVITSYWGIAVLAALPEFTFYETEEELFEE 180
QY 181 TICSALYPEDVYVSMRHFHTLMTIFCLVPLVMAICNGIITKTLRCPKSKRYKRIAL 240
DB 181 HSNHIFPYSFOQMKIFOLKTLNLGLVPLVMAICNGIITKTLRCPKSKRYKRIAL 240
QY 241 IFVIMAFLEFMTPPYNAVALLSYQSILFGNDCERSKHLDMVLTEVIAVSHCCANPVI 300
DB 241 IFVIMAFLEFMTPPYNAVALLSYQSILFGNDCERSKHLDMVLTEVIAVSHCCANPVI 300
QY 301 YAVGGERFKYLAHFRHLMHGRITPFLPSKLERTSSVSPSTAPELSIYF 355
DB 301 YAVGGERFKYLAHFRHLMHGRITPFLPSKLERTSSVSPSTAPELSIYF 355
DB 301 YAVGGERFKYLAHFRHLMHGRITPFLPSKLERTSSVSPSTAPELSIYF 355

+ RESULT 9
CCKLMOUSE STANDARD; PRT; 355 AA.
ID CCKLMOUSE STANDARD; PRT; 355 AA.
AC P51675;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1)
DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
DE (RANTES-R).
GN CCR1 OR CCR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=Peritoneal macrophage;
RX MEDLINE=96072806; PubMed=7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA Gerard C.;
RT "Molecular characterization of two murine eosinophil beta chemokine
RT receptors."
RL J. Immunol. 155:5299-5305(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=95340346; PubMed=7542241;
RA Gao J.-L., Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
RT beta chemokine receptor-like genes, including the gene for a
RT functional macrophage inflammatory protein-1 alpha receptor."

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RL J. Biol. Chem. 270:17494-17501(1995).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC RANTES, AND LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM ION LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
CC PROLIFERATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: DETECTED IN THE HEART, SPLEEN, LUNG,
CC PERITONEAL EXUDATE CELLS AND LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U29678; AAA86119.1; -
DR EMBL; U28404; AAA89153.1; -
DR MGI; 104618; Cmkrl1.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMAIN 224 239 6 (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 335 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT CONFILIT 55 M -> V (IN REF. 2).
SQ SEQUENCE 355 AA; 40901 MW; FCE9FEFF0E638B1 CRC64;

Query Match 60.1%; Score 1114.5; DB 1; Length 355;
Best Local Similarity 58.4%; Pred. No. 8,4e-57;
Matches 205; Conservative 63; Mismatches 82; Indels 1; Gaps 1;

QY 6 DIVEFGTSTYD-----DVGILCEKADTRALMAQFPPPLYSIVFTVGLGNVVMILLIYRR 64
DB 5 DFTFAVYPTTFEPYDSDTPCKTRAVRAGACLPLLSIVFTVGLGNVLMVLVLMKORR 64
QY 65 LRIMTNTIYLLNLTAISDLLELVLPFWIHVYRGHNVFGHGMCKILSGFHTGLYSEIFFI 124
DB 65 LQSWTSIYLFNLAVSDLVLEFPLFPWIDYKMDWMIGDMCKILSGFHTGLYSEIFFI 124
QY 125 ILTIDRYLAIVHAVPALARKYTFEGVITSYWGIAVLAALPEFTFYETEEELFEEPLCS 184
DB 125 ILTIDRYLAIVHAVPALARKYTFEGVITSYWGIAVLAALPEFTFYETEEELFEEPLCS 184
QY 185 ALYEPEDVYVSMRHFHTLMTIFCLVPLVMAICNGIITKTLRCPKSKRYKRIALRLEFI 244
DB 185 PHPPYKSLKOKKRRQALKNLGLILPLVMIICYAGIIRILRRPEKRYKAVRLFAI 244
QY 245 MAVFEIFMTPPYNAVALLSYQSILFGNDCERSKHLDMVLTEVIAVSHCCANPVIYAFV 304
DB 245 TLLEFLMTPTNYNLVSFAQDVLFTNQCQSKHLDMAMQVTEVIAVTHCCVNPVIYVFV 304
QY 305 GERFRKLRHFRHLMHGRITPFLPSKLERTSSVSPSTAPELSIYF 355

```


DB 305 GEFWKYRLQLEFORHVAIPALAKMLPFLSDQLERTSSISPSGHEHLSAGF 355

RESULT 10

CR2_RAT STANDARD: PRT: 373 AA.

AC 055193:

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C chemokine receptor type 2 (C-C CR-2) (CC-CR-2) (CCR-2) (CCR2).

GN CCR2 OR CCR2R.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OK NCBI_TaxID=10116;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RX MEDLINE=96318173; PubMed=9655467;

RA Jiang Y., Salafianca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K., deLebe C.M., Pennell N.A., Strelt W.J., Harrison J.K.;

RT "Chemokine receptor expression in cultured glia and rat experimental allergic encephalomyelitis.";

RT J. Neuroimmunol. 86:1-12(1998).

RL J. Neuroimmunol. 86:1-12(1998).

CC -1- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5 CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND MACROPHAGES.

CC -1- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----

DR EMBL: U77349; AAC03242.1;

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm.1.1.

DR PRINTS: PR00237; GPCR_RHODOPS.

DR PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; 1.

DR PROSITE: PS50262; G-PROTEIN_RECPT_F1_2; 1.

KV G-Protein coupled receptor; Transmembrane.

FT DOMAIN 1 60 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 61 81

FT DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 92 112 POTENTIAL.

FT DOMAIN 113 128 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 129 149 POTENTIAL.

FT DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 171 191 POTENTIAL.

FT DOMAIN 192 220 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 221 241 POTENTIAL.

FT DOMAIN 242 256 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 257 277 POTENTIAL.

FT DOMAIN 278 301 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 302 322 POTENTIAL.

FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).

FT DISULFID 126 203 BY SIMILARITY.

FT SEQUENCE 373 AA; 42763 MW; 2E7B012F5D6FD09 CRC64;

Query Match Score 963.5; DB 1; Length 373;

Best Local Similarity 53.0%; Pred. No. 3e-48;

Matches 187; Conservative 65; Mismatches 92; Indels 9; Gaps 7;

QY 4 SLIDVEFGTSTY-YDVGLCEKADPTALMAQFVPLYSIVFTVGLGNVYVWILLIKY 62

DB 25 STQELDEGATTPDYDD-GEPCHTSVKQIGAMWLPPLYSIVFTVGLGNVYVWILLIKY 83

QY 63 RLRLRTNYLLNLALISDLFLVTLPTFMVHYRGHNVYFGHGMCKLISGFTGLYSLEIF 122

DB 84 KKLKSMTDIYENLALISDLFLTLPLFMAHVA-ANEMVFGNIMCKLFLGVHIGVFGGIF 142

QY 123 FILLITIDRYLAIVAVNLRARVYGVYISYVWGLAVLAALPEFIYEEELFEETL 182

DB 143 FILLITIDRYLAIVAVNLRARVYGVYISYVWGLAVLAALPEFIYEEELFEETL 202

QY 183 GSALPEDEPVSWRPHLLRMVIFCLVPLVMAICYGIITLRCDS-KKKYAIRLI 241

DB 203 CGPIRP--TI--WKPFQIMRNILSLPLVMVVICIGILTLTRCKNEKRRARVLI 258

QY 242 FVIMAVFIETFPYVAVALLSSYOSILFGDCERSKHDLVLAALPEFIYEEELFEETL 301

DB 259 FAIMIVYELFWTPYVAVALLSSYOSILFGDCERSKHDLVLAALPEFIYEEELFEETL 318

QY 302 AFVGERFRKYLHFFHRLHMLGRVTPPLPESEKLERSSV-SPSTADELSI 353

DB 319 AFVGERFRKYLHFFHRLHMLGRVTPPLPESEKLERSSV-SPSTADELSI 371

RESULT 11

CR2_MOUSE STANDARD: PRT: 373 AA.

AC P51683; 061172;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE C-C chemokine receptor type 2 (C-C CR-2) (CC-CR-2) (CCR-2) (CCR2)

DE (JE/FIC receptor) (MCP-1 receptor).

GN CCR2 OR CCR2R.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OK NCBI_TaxID=10090;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=96205938; PubMed=8631787;

RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Teou C.-L., Charo I.F.;

RT "Molecular cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein 1alpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";

RT J. Biol. Chem. 271:7551-7558(1996).

RN (2)

RP SEQUENCE FROM N.A.

RC STRAIN=BALE/C;

RX MEDLINE=96216064; PubMed=8662823;

RA Kurihara T., Bravo R.;

RT "Cloning and functional expression of mCCR2, a murine receptor for the C-C chemokines JE and FIC.";

RT J. Biol. Chem. 271:11603-11606(1996).

RN (3)

RP SEQUENCE FROM N.A.

RX MEDLINE=97026720; PubMed=8872898;

RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R., Post T.W., Gerard C., Dorf M.E.;

RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse transcriptase-polymerase chain reaction does not detect mRNA for the KC or new MCP-1 receptor.";

RT J. Neurosci. Res. 45:382-391(1996).

RL J. Neurosci. Res. 45:382-391(1996).

CC -1- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5 CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES, BUT NOT IN NONHEMATOPOIETIC CELL LINES.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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DR EMBL: U47035; AAC52453.1; -
DR EMBL: U51717; AAC52557.1; -
DR EMBL: U56819; AAC52784.1; -
DR MGI: MGI:106185; Cnkb2.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 55
FT TRANSMEM 56 83
FT TRANSMEM 84 93
FT TRANSMEM 94 114
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FT TRANSMEM 37785 37839
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FT TRANSMEM 38055 38109
FT TRANSMEM 38109 38163
FT TRANSMEM 38163 38217
FT TRANSMEM 38217 38271
FT TRANSMEM 38271 38325
FT TRANSMEM 38325 38379
FT TRANSMEM 3837

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OY 133 LAIHAVALARARYTGVITISYWGIAVLAALPEFIETFEELFEELTCSALYEDTV 192
DB 140 LAIHAVALARARYTGVITISYWGIAVLAALPEFIETFEELFEELTCSALYEDTV 196
OY 193 XSMRPHRLMTIFCTVPLVMAICVYGIKTLRCPG-KKKYKAIPLIFMVFIE 251
DB 197 GMMNFHIMNITLGLVPLIMVICYGILTLCKRCKRHRVRLIFITMIVFLF 255
OY 252 WTPYVAILLSSYOSILGNDGERSKHLVLMVTEVIAVSHCCNMPYIAVGERFRKY 311
DB 256 WTPYVAILLSSYOSILGNDGERSKHLVLMVTEVIAVSHCCNMPYIAVGERFRKY 315
OY 312 LRHFPHRLMHLGRTYIFPLSEKER-TSSVSPTAPELSI 353
DB 316 LSMFPRKTYTKRCKQCPVYREIVDVTSTWTFSTAOEVSV 358

RESULT 13
CRR5_MACMU
ID CRR5_MACMU STANDARD: PRT: 352 AA.
AC P79436: 002746;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CCR5R.
OS Macaca mulatta (rhesus macaque),
OS Macaca fascicularis (Crisp eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID:9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-M.mulatta;
RX MEDLINE-97184592; PubMed-9032394;
RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA Newman W., Gerard N., Gerard C., Sodroski J.;
RT "Utilization of C-C chemokine receptor 5 by the envelope
RT glycoproteins of a pathogenic simian immunodeficiency virus,
RT siymac239."
RT J. Virol. 71:2522-2527(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-M.mulatta; STRAIN-Indian macaque;
RX MEDLINE-97213934; PubMed-9060623;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT "Genetically divergent strains of simian immunodeficiency virus use
RT CCR5 as a coreceptor for entry."
RT J. Virol. 71:2705-2714(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-M.mulatta;
RX MEDLINE-21354176; PubMed-11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."
RT AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-M.mulatta, M.fascicularis, and M.nemestrina;
RX MEDLINE-97268687; PubMed-9108095;
RA Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RT Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1 ALPHA,
CC MIP-1 BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR

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CC DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
DR EMBL: U77672; AAC51109.1; -
DR EMBL: U73739; AAC51158.1; -
DR EMBL: U96762; AAC34132.1; -
DR EMBL: AF005660; AAB62554.1; -
DR EMBL: AF005661; AAB62555.1; -
DR EMBL: AF005662; AAB62556.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFD 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT CARBOHYD 268 268
FT CONFLICT 241 241
FT CONFLICT 292 292
SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;
Query Match 51.2%; Score 949.5; DB 1; Length 352;
Best Local Similarity 54.5%; Pred. No. 1.8e-47;
Matches 181; Conservative 58; Mismatches 90; Indels 3; Gaps 3;
OY 24 CEKADTALMAQVFPPLXSLVTVGLGNGVVVYMLITRYRRLRINTYILNLTATSDLF 83
DB 20 CQKIVKQIARLRLPLXSLVTVFSGVNLVLLINCKRKSTDTYLLNLTATSDLF 79
OY 84 LVLPFWIHYVGNHNVFGHGCKLLSGPYRTGLYSEIFITLLTIDRYALIVAAVPAIR 143
DB 80 LLTVFPMHAYAA -QMDFGNTMCQLLTGLYIGFSGIFETILLTIDRYALIVAAVPAIR 138
OY 144 ARTVFGVITISYWGIAVLAALPEFIETFEELFEELTCSALYEDTVYSKRHHITRM 203
DB 139 ARTVFGVITISYWGIAVLAALPEFIETFEELFEELTCSALYEDTVYSKRHHITRM 198
OY 204 TIFCVLPLVLAICVYGIKTLRCPG-KKKYKAIPLIFMVFIEFTMPPYVAAILLS 262
DB 199 VILGLVPLVLAICVYGIKTLRCPG-KKKYKAIPLIFMVFIEFTMPPYVAAILLS 258
OY 263 SYOSILGNDGERSKHLVLMVTEVIAVSHCCNMPYIAVGERFRKYLRHFPHRLM 322
DB 259 TQGEFFGLNCSNRRLDQAVTVETLGMTHCCINPIIYAFGEFRNYLLVFPQKIAK 318

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OY 323 HGNRIPLPSEKERTSSV-SPSTAPELSTI 353
 DB 319 RFCCKCSIFQOEAPERASSVYTRSTGEISV 350
 RESULT 14
 CCR5_HYLL
 ID CCR5_HYLL STANDARD: PRT: 352 AA.
 AC 097883;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5B5.
 OS Hylobates leucogenys (White-cheeked gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylodactylidae; Hylobates.
 OX NCBI_TaxId=61853;
 RP [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-99416438; PubMed-10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: AF075451; AAD19863.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECPT_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSSEM 31 58
 FT TRANSSEM 59 68
 FT TRANSSEM 69 89
 FT DOMAIN 90 102
 FT TRANSSEM 103 124
 FT DOMAIN 125 141
 FT TRANSSEM 142 166
 FT TRANSSEM 167 198
 FT TRANSSEM 199 218
 FT TRANSSEM 219 235
 FT DOMAIN 236 260
 FT TRANSSEM 261 277
 FT TRANSSEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD_RSS 3 3
 FT MOD_RSS 10 10
 FT MOD_RSS 14 14
 FT SEQUENCE 352 AA; 40445 MW; 4F8EAF344CEB7C91 CRC64;
 Query Match 51.18; Score 948; DB 1; Length 352;
 Best Local Similarity 52.98; Pred. No. 2.1e-47;
 Matches 181; Conservative 62; Mismatches 93; Indels 6; Gaps 4;
 OY 17 YD--DVGLCEKADTRALMAQFVPLYSLVFTVGLGNVYVWILLKRYRLRLMTNTNYL 73

DB 10 YDIDYDSEPOCKINVAQIARLLPPLYSLVFIFGVGNMVLIVLINCRLKSMETDIYL 69
 OY 74 LNLALSDLLFLVTLPEFMHYRGHNVPGHCKMLLSGFYHTGLXSELPFIILITDRL 133
 DB 70 LNLALSDLLFLVTLPEFMHYRGHNVPGHCKMLLSGFYHTGLXSELPFIILITDRL 128
 OY 134 ALVAVPALRARVTFGVITSIVTWGLAVLALPEEFYETEELFEETLCSALYEDPTVY 193
 DB 129 ALVAVPALRARVTFGVITSIVTWGLAVLALPEEFYETEELFEETLCSALYEDPTVY 188
 OY 194 SWRHFTLRMTIFELVPLVMAICYGIITLRCDS-KKKYAIRLIFVYNAVFLEW 252
 DB 189 FKNKFOELKIVILVPLVMAICYGIITLRCDS-KKKYAIRLIFVYNAVFLEW 248
 OY 253 TPYVAVLISYOSILGNCDESKHLDVLTVEVLAISHCQNNPVYAFVGRPRYL 312
 DB 249 APYIVILLNTFOEFGGLNCSNRLDQAAQVETVGMTHCCINPIITVAFVGRPRYL 308
 OY 313 RHFFRHLLMHLGRYIPFLPSEKERTSSV-SPSTAPELSTI 353
 DB 309 LVFQKHAKRPFCKCSIFQOEAPERASSVYTRSTGEISV 350
 RESULT 15
 CCR5_CERAE
 ID CCR5_CERAE STANDARD: PRT: 352 AA.
 AC P56493;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
 GN Cercopithecus aethiops (Green monkey) (Givet).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxId=9534;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE-Kidney;
 RX MEDLINE-98001387; PubMed-934322;
 RA Kulmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 implicate specific amino acids in infections by simian and human
 immunodeficiency viruses.";
 RL J. Virol. 71:8642-8656(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
 RT "CDNA sequence of African green monkey CCR-5 chemokine receptor
 gene.";
 RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
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 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
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 CC -----
 DR EMBL: U83324; AAC51795.1;
 DR EMBL: U83325; AAC51796.1;
 DR EMBL: AB015944; BAA31328.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.

